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SEQUENCE LISTING

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 Murdin, Andrew

<120> Chlamydia mgp002

<130> APL-03-03-PCT

<150> 60/481,690
 <151> 2003-11-21

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<170> PatentIn version 3.3

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 Ser Thr Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala
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 aag tca tac tta caa caa agt ctc ttt tct gaa gat gct tac gta cgc 240
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 Lys Ser Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu
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Ala Thr Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile
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 Ser Lys Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys
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Gln Lys Ser Ile Pro Gln Ala Leu Glu Ser Tyr Leu Glu Ala Ser Thr
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Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala Lys Ser
35 40 45
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Ser Lys Ser Asn Pro Glu Val Ala Leu Ala Ala Ala Gln Thr Leu Leu				
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Gln Phe Trp Lys Glu Cys Thr Ala Leu Pro Leu Leu Ser Pro Glu Glu				
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aaa gca aga gct ttg gca atg tat cgc gca gca gaa gat acg atc ctc				1152

370	375	380	
tct agt tta tta aaa tta cct aac aat gcc tat ctg cct tat ttg gaa Ser Ser Leu Leu Lys Leu Pro Asn Asn Ala Tyr Leu Pro Tyr Leu Glu 385 390 395 400			1200
cgt att cta act tca caa aaa acc cct cta gca gct aaa gct att gct Arg Ile Leu Thr Ser Gln Lys Thr Pro Leu Ala Ala Lys Ala Ile Ala 405 410 415			1248
ttt tta tca gta aca gct cat cct cag gca ctt tct tta gtc tcg aaa Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys 420 425 430			1296
gca gca cta act cca gga gac cct atc att cgc gct tat gcg aat tta Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu 435 440 445			1344
gct tta tat aca atg acg caa gat cct gaa aag aaa gcc tta tta tat Ala Leu Tyr Thr Met Thr Gln Asp Pro Glu Lys Lys Ala Leu Leu Tyr 450 455 460			1392
caa tat gcc gaa cag tta ata gga gac acg att ttg ttt aca gat gag Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr Asp Glu 465 470 475 480			1440
gag aat ccc ctg cct tct ccc cat tct tcc tac ctg cga tat caa gtg Glu Asn Pro Leu Pro Ser Pro His Ser Ser Tyr Leu Arg Tyr Gln Val 485 490 495			1488
tcc cca gaa act cgt tct caa ctc atg cta act att tta gaa acc cta Ser Pro Glu Thr Arg Ser Gln Leu Met Leu Thr Ile Leu Glu Thr Leu 500 505 510			1536
gtt tct tct aaa act gat gaa gac atc cga gtt ttt ctt tcg cta atg Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met 515 520 525			1584
aaa aaa acc cat tac aaa aat atc ccc atc tta tct gga tta tta atg Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met 530 535 540			1632
aga ata gtg gag cga gct cgg tac caa gct tac gta gaa caa aaa ctc Arg Ile Val Glu Arg Ala Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu 545 550 555 560			1680
atc tca gaa gag gat Ile Ser Glu Glu Asp 565			1695

<210> 6
 <211> 565
 <212> PRT
 <213> Chlamydia muridarum

Met Cys Asp Phe Pro Pro Ser Val Ser Gln Lys Ile Leu Phe Leu Cys
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 Gln Lys Ser Ile Pro Gln Ala Leu Glu Ser Tyr Leu Glu Ala Ser Thr
 20 25 30
 Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala Lys Ser
 35 40 45
 Tyr Leu Gln Gln Ser Leu Phe Ser Glu Asp Ala Tyr Val Arg Lys Ser
 50 55 60
 Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu Asp Leu
 65 70 75 80
 Leu Ser Glu Ser Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu Leu Ile
 85 90 95
 Leu Asn Ala Ala Gly Asn Gln Leu Gly Lys Thr Ser Asp Arg Leu Leu
 100 105 110
 Phe Lys Gly Leu Thr Ala Pro His Pro Ile Ile Arg Leu Glu Ala Ala
 115 120 125
 Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr
 130 135 140
 Ser Phe Ile His Gln Leu Pro Glu Glu Ile Gln Asn Leu Ala Ala Thr
 145 150 155 160
 Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Val His Arg
 165 170 175
 Leu Leu Ser Ser Pro Asn Ser Leu Thr Arg Asn Tyr Met Ala Tyr Leu
 180 185 190
 Ile Gly Glu Tyr Gln Gln Arg Arg Phe Leu Pro Thr Leu Arg Ser Leu
 195 200 205
 Leu Thr Ser Ala Ala Pro Leu Asp Gln Glu Gly Ser Leu Tyr Ala Ile
 210 215 220

Gly Lys Leu Glu Asp Ala Ser Ser Tyr Pro Lys Ile Lys Ala Leu Ser
 225 230 235 240
 Ser Lys Ser Asn Pro Glu Val Ala Leu Ala Ala Ala Gln Thr Leu Leu
 245 250 255
 Phe Leu Gly Lys Glu Asp Glu Ala Leu Pro Ile Leu Thr Thr Phe Cys
 260 265 270
 Gln Gln Glu Leu Pro Arg Ala Ile Tyr Thr Ser Arg Phe Leu Ser Leu
 275 280 285
 Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Cys Lys Ala Ile Lys
 290 295 300
 Glu Glu Ile Lys Leu Asn Ala Ala Leu Ala Leu Val His Leu Gly Ser
 305 310 315 320
 Val Asn His Leu Val Leu Ser Tyr Leu Thr Glu Phe Leu Glu Asn Lys
 325 330 335
 Ile Leu His Arg Ile Phe Leu Pro Thr His Ser Ile Gly Lys Ala Thr
 340 345 350
 Gln Phe Trp Lys Glu Cys Thr Ala Leu Pro Leu Leu Ser Pro Glu Glu
 355 360 365
 Lys Ala Arg Ala Leu Ala Met Tyr Arg Ala Ala Glu Asp Thr Ile Leu
 370 375 380
 Ser Ser Leu Leu Lys Leu Pro Asn Asn Ala Tyr Leu Pro Tyr Leu Glu
 385 390 395 400
 Arg Ile Leu Thr Ser Gln Lys Thr Pro Leu Ala Ala Lys Ala Ile Ala
 405 410 415
 Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys
 420 425 430
 Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu
 435 440 445

Ala Leu Tyr Thr Met Thr Gln Asp Pro Glu Lys Lys Ala Leu Leu Tyr
 450 455 460

Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr Asp Glu
 465 470 475 480

Glu Asn Pro Leu Pro Ser Pro His Ser Ser Tyr Leu Arg Tyr Gln Val
 485 490 495

Ser Pro Glu Thr Arg Ser Gln Leu Met Leu Thr Ile Leu Glu Thr Leu
 500 505 510

Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met
 515 520 525

Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met
 530 535 540

Arg Ile Val Glu Arg Ala Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu
 545 550 555 560

Ile Ser Glu Glu Asp
 565

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 <212> DNA
 <213> Chlamydia trachomatis

<220>
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 cga aaa tca gtc cct caa gct cta gaa gcc tat ctc gaa gct tca gca 96
 Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala Ser Ala
 20 25 30
 act tat caa caa cac gat ttc tcc gta tta cgc gta ata gca gaa tcg 144
 Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala Glu Ser
 35 40 45

Tyr	Leu	Gln	Gln	Ser	Phe	Leu	Ser	Glu	Asp	Thr	Tyr	Ile	Arg	Lys	Ser		
50						55					60						
gca	att	att	gga	gca	ggg	cta	tct	ggt	tca	tca	gaa	gct	tta	gag	tta	240	
Ala	Ile	Ile	Gly	Ala	Gly	Leu	Ser	Gly	Ser	Ser	Glu	Ala	Leu	Glu	Leu		
65					70				75					80			
ctg	tct	gag	gct	ata	gaa	acg	caa	gat	ctc	tat	gag	caa	cta	ctc	att	288	
Leu	Ser	Glu	Ala	Ile	Glu	Thr	Gln	Asp	Leu	Tyr	Glu	Gln	Leu	Leu	Ile		
				85				90					95				
tta	aat	gct	gca	acc	agc	caa	tta	agc	aaa	act	tct	gac	aaa	ctt	tta	336	
Leu	Asn	Ala	Ala	Thr	Ser	Gln	Leu	Ser	Lys	Thr	Ser	Asp	Lys	Leu	Leu		
			100					105					110				
ttc	aag	gga	tta	aca	gct	tct	cat	cct	gtc	atc	cgc	tta	gaa	gct	gct	384	
Phe	Lys	Gly	Leu	Thr	Ala	Ser	His	Pro	Val	Ile	Arg	Leu	Glu	Ala	Ala		
		115					120					125					
tat	cgt	ctt	gcc	tgt	atg	aaa	aat	agc	aag	gta	agt	gat	tac	ctt	tat	432	
Tyr	Arg	Leu	Ala	Cys	Met	Lys	Asn	Ser	Lys	Val	Ser	Asp	Tyr	Leu	Tyr		
	130					135				140							
tct	ttt	atc	tac	aag	tta	cca	gaa	gaa	att	caa	aac	cta	gcg	gca	act	480	
Ser	Phe	Ile	Tyr	Lys	Leu	Pro	Glu	Glu	Ile	Gln	Asn	Leu	Ala	Ala	Thr		
145					150				155					160			
att	ttc	tta	caa	ctc	gaa	aca	gaa	gaa	gct	gat	gct	tat	att	cat	cat	528	
Ile	Phe	Leu	Gln	Leu	Glu	Thr	Glu	Glu	Ala	Asp	Ala	Tyr	Ile	His	His		
				165				170						175			
ttg	ctc	tct	tct	ccc	aat	aac	ctg	aca	aga	aac	tat	gtt	gcc	tat	tta	576	
Leu	Leu	Ser	Ser	Pro	Asn	Asn	Leu	Thr	Arg	Asn	Tyr	Val	Ala	Tyr	Leu		
			180					185					190				
att	gga	gag	tac	aaa	caa	aaa	aga	ttt	ctt	cca	aca	cta	cgc	tct	tta	624	
Ile	Gly	Glu	Tyr	Lys	Gln	Lys	Arg	Phe	Leu	Pro	Thr	Leu	Arg	Ser	Leu		
		195					200					205					
ctt	aca	agt	gcc	tct	cct	tta	gat	caa	gaa	ggc	gct	ttg	tat	gcg	tta	672	
Leu	Thr	Ser	Ala	Ser	Pro	Leu	Asp	Gln	Glu	Gly	Ala	Leu	Tyr	Ala	Leu		
	210					215					220						
ggc	aaa	ctg	gaa	gac	tct	ggt	agc	tat	cct	aga	att	aaa	gct	cta	agc	720	
Gly	Lys	Leu	Glu	Asp	Ser	Gly	Ser	Tyr	Pro	Arg	Ile	Lys	Ala	Leu	Ser		
225					230				235					240			
tct	aga	tcc	aat	cct	gaa	gta	gta	ctc	gct	gca	gct	cag	aca	tta	tta	768	
Ser	Arg	Ser	Asn	Pro	Glu	Val	Val	Leu	Ala	Ala	Ala	Gln	Thr	Leu	Leu		
				245				250						255			
ttc	tta	gag	aaa	gaa	gaa	gaa	gct	cta	ccg	atc	cta	acc	aac	ctt	tgc	816	
Phe	Leu	Glu	Lys	Glu	Glu	Glu	Ala	Leu	Pro	Ile	Leu	Thr	Asn	Leu	Cys		
			260				265						270				
caa	caa	aaa	ctt	ctt	cga	gcc	ctg	tat	acc	gca	cgt	ttc	ctc	tcg	caa	864	

275	280	285	
gag aag ggt gaa gag ctt ctt ctt cca atc ttt tat aac gca aca caa Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Tyr Asn Ala Thr Gln 290 295 300			912
gaa gaa att aga ctg aat act gct tta gca ctt gtt cat caa ggg tgt Glu Glu Ile Arg Leu Asn Thr Ala Leu Ala Leu Val His Gln Gly Cys 305 310 315 320			960
aca gat cct caa gtc ctc cac tat cta aca gaa atc tta gaa agt aaa Thr Asp Pro Gln Val Leu His Tyr Leu Thr Glu Ile Leu Glu Ser Lys 325 330 335			1008
gtt ctc cat cgc ata ttt tta cct act cac tcg aca gga aaa gct ata Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys Ala Ile 340 345 350			1056
cag ttc tgg aaa gaa tgc acc act ttt cct ctc atg agc caa gaa gac Gln Phe Trp Lys Glu Cys Thr Thr Phe Pro Leu Met Ser Gln Glu Asp 355 360 365			1104
aaa atg aga acg ttg gct atg tat cgg gta gcg gaa gat acc atc ctc Lys Met Arg Thr Leu Ala Met Tyr Arg Val Ala Glu Asp Thr Ile Leu 370 375 380			1152
tca gcg tta cta aaa tta ccc aat gac gcc tat ctt cct tac cta gag Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr Leu Glu 385 390 395 400			1200
cgc atc ctc gcc tca caa aaa act ata cta gca gct aaa gct att gct Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala Ile Ala 405 410 415			1248
ttt tta tcg gta aca gct cat cct cag gca ctt tct tta gtc tcg aaa Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys 420 425 430			1296
gct gca tta act cct gga gac cct atc att cgc gct tac gct aat cta Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu 435 440 445			1344
gct tta tat aca atg acc aaa gat cct gag aaa aaa gct gtg cta tac Ala Leu Tyr Thr Met Thr Lys Asp Pro Glu Lys Lys Ala Val Leu Tyr 450 455 460			1392
cga tat gct gaa caa tta ata gag gat acc att tta ttc aca gat gct Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr Asp Ala 465 470 475 480			1440
gaa aat ccg ctt ccc tct cca agc tct tct tat tta cgc tac caa gta Glu Asn Pro Leu Pro Ser Pro Ser Ser Tyr Leu Arg Tyr Gln Val 485 490 495			1488
tcc cct gag acc cgc aca caa ctt atg cta gct att ttg gaa acc tta Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu Thr Leu 500 505 510 515 520			1536

gtt tct tcc aaa acg gat gaa gat atc cgc gtt ttt ctt tcc cta atg 1584
 Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met
 515 520 525

aaa aaa acc cat tac aaa aat atc ccg atc tta tca gga ttg tta atg 1632
 Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met
 530 535 540

aga ata gtg gag 1644
 Arg Ile Val Glu
 545

<210> 8
 <211> 548
 <212> PRT
 <213> Chlamydia trachomatis

<400> 8

Met Cys Asp Phe Pro Ser Ser Val Ser Gln Arg Ile Leu Phe Ser Cys
 1 5 10 15

Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala Ser Ala
 20 25 30

Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala Glu Ser
 35 40 45

Tyr Leu Gln Gln Ser Phe Leu Ser Glu Asp Thr Tyr Ile Arg Lys Ser
 50 55 60

Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Ala Leu Glu Leu
 65 70 75 80

Leu Ser Glu Ala Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu Leu Ile
 85 90 95

Leu Asn Ala Ala Thr Ser Gln Leu Ser Lys Thr Ser Asp Lys Leu Leu
 100 105 110

Phe Lys Gly Leu Thr Ala Ser His Pro Val Ile Arg Leu Glu Ala Ala
 115 120 125

Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr
 130 135 140

Ser Phe Ile Tyr Lys Leu Pro Glu Glu Ile Gln Asn Leu Ala Ala Thr
 145 150 155 160
 Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile His His
 165 170 175
 Leu Leu Ser Ser Pro Asn Asn Leu Thr Arg Asn Tyr Val Ala Tyr Leu
 180 185 190
 Ile Gly Glu Tyr Lys Gln Lys Arg Phe Leu Pro Thr Leu Arg Ser Leu
 195 200 205
 Leu Thr Ser Ala Ser Pro Leu Asp Gln Glu Gly Ala Leu Tyr Ala Leu
 210 215 220
 Gly Lys Leu Glu Asp Ser Gly Ser Tyr Pro Arg Ile Lys Ala Leu Ser
 225 230 235 240
 Ser Arg Ser Asn Pro Glu Val Val Leu Ala Ala Ala Gln Thr Leu Leu
 245 250 255
 Phe Leu Glu Lys Glu Glu Glu Ala Leu Pro Ile Leu Thr Asn Leu Cys
 260 265 270
 Gln Gln Lys Leu Leu Arg Ala Leu Tyr Thr Ala Arg Phe Leu Ser Gln
 275 280 285
 Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Tyr Asn Ala Thr Gln
 290 295 300
 Glu Glu Ile Arg Leu Asn Thr Ala Leu Ala Leu Val His Gln Gly Cys
 305 310 315 320
 Thr Asp Pro Gln Val Leu His Tyr Leu Thr Glu Ile Leu Glu Ser Lys
 325 330 335
 Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys Ala Ile
 340 345 350
 Gln Phe Trp Lys Glu Cys Thr Thr Phe Pro Leu Met Ser Gln Glu Asp
 355 360 365

370 375 380
 Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr Leu Glu
 385 390 395 400
 Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala Ile Ala
 405 410 415
 Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys
 420 425 430
 Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu
 435 440 445
 Ala Leu Tyr Thr Met Thr Lys Asp Pro Glu Lys Lys Ala Val Leu Tyr
 450 455 460
 Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr Asp Ala
 465 470 475 480
 Glu Asn Pro Leu Pro Ser Pro Ser Ser Ser Tyr Leu Arg Tyr Gln Val
 485 490 495
 Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu Thr Leu
 500 505 510
 Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met
 515 520 525
 Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met
 530 535 540
 Arg Ile Val Glu
 545

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 <213> Chlamydia trachomatis

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41

<210> 10
<211> 40
<212> DNA
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<400> 10
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40

<210> 11
<211> 41
<212> DNA
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<400> 11
ataagaatgc ggccgccacc atgtgcgact tccccccag t

41

<210> 12
<211> 40
<212> DNA
<213> Chlamydia trachomatis

<400> 12
gttggtaccg agctcgctcc actattctca ttaataatcc

40

<210> 13
<211> 31
<212> DNA
<213> Chlamydia trachomatis

<400> 13
gaattcggat ccgatgggat tatctcgct a

31

<210> 14
<211> 36
<212> DNA
<213> Chlamydia trachomatis

<400> 14
attaagaatg cggccgcttt atcactccac tattct

36